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Figure 1A SEQ ID No 1.

1 GAGGTCCAGC TTCAGCAGTC TGGACCTGAC CTGGTGAAGC CTGGGGCTTC
E V Q L Q Q S G P D L V K P G A S

51 AGTGAAGATA TCCTGCAAGG CTTCTGGTTA CTCATTCACT GGCTACTACA
V K I S C K A S G Y S F T G Y Y

101 TGCACCTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGACGT
M H W V K Q S H G K S L E W I G R

151 ATTAATCCTA ACAATGGTGT TACTCTCTAC AACCAGAAAT TCAAGGACAA
I N P N N G V T L Y N Q K F K D K

201 GGCCATATTA ACTGTAGACA AGTCATCCAC CACAGCCTAC ATGGAGCTCC
A I L T V D K S S T T A Y M E L

251 GCAGCCTGAC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGATCTACT
R S L T S E D S A V Y Y C A R S T

301 ATGATTACGA ACTATGTTAT GGACTIONG GGTCAAGTAA CCTCAGTCAC
M I T N Y V M D Y W G Q V T S V T

351 CGTCTCCTCA GGTGGTGGTG GGAGCGGTGG TGGCGGCACT GGCAGCGGCG
V S S G G G G S G G G G T G G G

401 GATCTAGTAT TGTGATGACC CAGACTCCCA CATTCTGCT TGTTCAGCA
G S S I V M T Q T P T F L L V S A

451 GGAGACAGGG TTACCATAAC CTGCAAGGCC AGTCAGAGTG TGAGTAATGA
G D R V T I T C K A S Q S V S N D

501 TGTAGDTTGG TACCAACAGA AGCGAGGGCA GTCTCCTACA CTGCTCATAT
V A W Y Q Q K P G Q S P T L L I

551 CCTATACATC CAGTCGCTAC GCTGGAGTCC CTGATCGCTT CATTGGCAGT
S Y T S S R Y A G V P D R F I G S

601 GGATATGGGA CGGATTTCAC TTTCACCATC AGCACTTTGC AGGCTGAAGA
G Y G T D F T F T I S T L Q A E D

651 CCTGGCAGTT TATTTCTGTC AGCAAGATTA TAATTCTCCT CCGACGTTCC
L A V Y F C Q Q D Y N S P P T F

701 GTGGAGGCAC CAAGCTGGAA ATCAAACGG
G G G T K L E I K R

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Figure 1B SEQ ID No 2.

1 AAGCTTCCAC CATGGGATGG AGCTGTATCA TCCTCTTCTT GGTAGCAACA
A S T M G W S C I I L F L V A T

51 GCTACAGGTG TCCACTCCGA GGTCCAGCTT CAGCAGTCTG GACCTGACCT
A T G V H S E V Q L Q Q S G P D L

101 GGTGAAGCCT GGGGCTTCAG TGAAGATATC CTGCAAGGCT TCTGGTTACT
V K P G A S V K I S C K A S G Y

151 CATTCACTGG CTACTACATG CACTGGGTGA AGCAGAGCCA TGGAAAGAGC
S F T G Y Y M H W V K Q S H G K S

201 CTTGAGTGGA TTGGACGTAT TAATCCTAAC AATGGTGTTA CTCTCTACAA
L E W I G R I N P N N G V T L Y N

251 CCAGAAATTC AAGGACAAGG CCATATTAAC TGTAACAAG TCATCCACCA
Q K F K D K A I L T V D K S S T

301 CAGCCTACAT GGAGCTCCGC AGCCTGACAT CTGAGGACTC TGCGGTCTAT
T A Y M E L R S L T S E D S A V Y

351 TACTGTGCAA GATCTACTAT GATTACGAAC TATGTTATGG ACTACTGGGG
Y C A R S T M I T N Y V M D Y W G

401 TCAAGTAACC TCAGTCACCG TCTCCTCAGG TGGTGGTGGG AGCGGTGGTG
Q V T S V T V S S G G G G S G G

451 GCGGCACTGG CGGCGGCGGA TCTAGTATTG TGATGACCCA GACTCCCACA
G G T G G G G S S I V M T Q T P T

501 TTCCTGCTTG TTTCAGCAGG AGACAGGGTT ACCATAACCT GCAAGGCCAG
F L L V S A G D R V T I T C K A S

551 TCAGAGTGTG AGTAATGATG TAGCTTGGTA CCAACAGAAG CCAGGGCAGT
Q S V S N D V A W Y Q Q K P G Q

601 CTCCTACACT GCTCATATCC TATACATCCA GTCGCTACGC TGGAGTCCCT
S P T L L I S Y T S S R Y A G V P

651 GATCGCTTCA TTGGCAGTGG ATATGGGACG GATTTCACTT TCACCATCAG
D R F I G S G Y G T D F T F T I S

701 CACTTTGCAG GCTGAAGACC TGGCAGTTTA TTTCTGTCAG CAAGATTATA
T L Q A E D L A V Y F C Q Q D Y

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751 ATTCTCCTCC GACGTTCTGGT GGAGGCACCA AGCTGGAAAT CAAACGGGCC
N S P P T F G G G T K L E I K R A

801 TCCACCAAGG GCCCATCTGGT CTTCCCCCTG GCACCCTCCT CCAAGAGCAC
S T K G P S V F P L A P S S K S T

851 CTCTGGGGGC ACAGCGGCCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG
S G G T A A L G C L V K D Y F P

901 AACCGGTGAC GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC
E P V T V S W N S G A L T S G V H

951 ACCTTCCCGG CTGTCCTACA GTCCTCAGGA CTCTACTCCC TCAGCAGCGT
T F P A V L Q S S G L Y S L S S V

1001 GGTGACCGTG CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG
V T V P S S S L G T Q T Y I C N

1051 TGAATCACAA GCCCAGCAAC ACCAAGGTGG ACAAGAAAGT TGAGCCCCAA
V N H K P S N T K V D K K V E P K

1101 TCTTGTGACA AAACTCACAC ATGCCCACCG TGCCCAGCAC CTGAACTCCT
S C D K T H T C P P C P A P E L L

1151 GGGGGGACCG TCAGTCTTCC TCTTCCCCC AAAACCCAAG GACACCCTCA
G G P S V F L F P P K P K D T L

1201 TGATCTCCCG GACCCCTGAG GTCACATGCG TGGTGGTGGG CGTGAGCCAC
M I S R T P E V T C V V V D V S H

1251 GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG TGGAGGTGCA
E D P E V K F N W Y V D G V E V H

1301 TAATGCCAAG-ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGTG
N A K T K P R E E Q Y N S T Y R

1351 TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAG
V V S V L T V L H Q D W L N G K E

1401 TACAAGTGCA AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TCGAGAAAAC
Y K C K V S N K A L P A P I E K T

1451 CATCTCCAAA GCCAAAGGGC AGCCCCGAGA ACCACAGGTG TACACCCTGC
I S K A K G Q P R E P Q V Y T L

1501 CCCCATCCCG GGATGAGCTG ACCAAGAACC AGGTCAGCCT GACCTGCCTG
P P S R D E L T K N Q V S L T C L

1801 CAAGCTT
P S

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Figure 2. SEQ ID No3.

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CAATTTCTTT CAGCTCTTGG TGCTGGCTGG TCTTTCTCAC TTCTGTTTCA	100
N F F Q L L V L A G L S H F C S	
GTGTTATCCA CGTGACCAAG GAAGTGAAAG AAGTGGCAAC GCTGTCCTGT	150
G V I H V T K E V K E V A T L S C	
GGTCACAATG TTTCTGTTGA AGAGCTGGCA CAAACTCGCA TCTACTGGCA	200
G H N V S V E E L A Q T R I Y W Q	
AAAGGAGAAG AAAATGGTGC TGAATATGAT GTCTGGGGAC ATGAATATAT	250
K E K K M V L T M M S G D M N I	
GGCCCGAGTA CAAGAACCGG ACCATCTTTG ATATCACTAA TAACCTCTCC	300
W P E Y K N R T I F D I T N N L S	
ATTGTGATCC TGGCTCTGCG CCCATCTGAC GAGGGCACAT ACGAGTGTGT	350
I V I L A L R P S D E G T Y E C V	
TGTTCTGAAG TATGAAAAAG ACGCTTTCAA GCGGGAACAC CTGGCTGAAG	400
V L K Y E K D A F K R E H L A E	
TGACGTTATC AGTCAAAGCT GACTTCCCTA CACCTAGTAT ATCTGACTTT	450
V T L S V K A D F P T P S I S D F	
GAAATTCCAA CTTCTAATAT TAGAAGGATA ATTTGCTCAA CCTCTGGAGG	500
E I P T S N I R R I I C S T S G G	
TTTTCCAGAG CCTCACCTCT CCTGGTTGGA AAATGGAGAA GAATTAAATG	550
F P E P H L S W L E N G E E L N	
CCATCAACAC AACAGTTTCC CAAGATCCTG AAAGTGAAGT CTATGCTGTT	600
A I N T T V S Q D P E T E L Y A V	
AGCAGCAAAC TGGATTTCAT TATGACAACC AACCACAGCT TCATGTGTCT	650
S S K L D F N M T T N H S F M C L	
CATCAAGTAT GGACATTTAA GAGTGAATCA GACCTTCAAC TGGAATACAA	700
I K Y G H L R V N Q T F N W N T	

CCAAGCAAGA GCATTTTCCT GATGGAGGCG GGGGATCCGA GGTCCAGCTT 750
T K Q E H F P D G G G G S E V Q L

CAGCAGTCTG GACCTGACCT GGTGAAGCCT GGGGCTTCAG TGAAGATATC 800
Q Q S G P D L V K P G A S V K I S

CTGCAAGGCT TCTGGTTACT CATTCACTGG CTACTACATG CACTGGGTGA 850
C K A S G Y S F T G Y Y M H W V

AGCAGAGCCA TGGAAAGAGC CTTGAGTGGA TTGGACGTAT TAATCCTAAC 900
K Q S H G K S L E W I G R I N P N

AATGGTGTTA CTCTCTACAA CCAGAAATTC AAGGACAAGG CCATATTAAC 950
N G V T L Y N Q K F K D K A I L T

TGTAGACAAG TCATCCACCA CAGCCTACAT GGAGCTCCGC AGCCTGACAT 1000
V D K S S T T A Y M E L R S L T

CTGAGGACTC TGCGGTCTAT TACTGTGCAA GATCTACTAT GATTACGAAC 1050
S E D S A V Y Y C A R S T M I T N

TATGTTATGG ACTACTGGGG TCAAGTAACC TCAGTCACCG TCTCCTCAGG 1100
Y V M D Y W G Q V T S V T V S S G

TGGTGGTGGG AGCGGTGGTG GCGGCACTGG CGGCGGCGGA TCTAGTATTG 1150
G G G S G G G G T G G G G S S I

TGATGACCCA GACTCCCACA TTCCTGCTTG TTTCAGCAGG AGACAGGGTT 1200
V M T Q T P T F L L V S A G D R V

ACCATAACCT GCAAGGCCAG TCAGAGTGTG AGTAATGATG TAGCTTG GTA 1250
T I T C K A S Q S V S N D V A W Y

CCAACAGAAG CCAGGGCAGT CTCCTACACT GCTCATATCC TATACATCCA 1300
Q Q K P G Q S P T L L I S Y T S

GTCGCTACGC TGGAGTCCCT GATCGCTTCA TTGGCAGTGG ATATGGGACG 1350
S R Y A G V P D R F I G S G Y G T

GATTTCACTT TCACCATCAG CACTTTGCAG GCTGAAGACC TGGCAGTTTA 1400
D F T F T I S T L Q A E D L A V Y

TTTCTGTCAG CAAGATTATA ATTCTCCTCC GACGTTCCGT GGAGGCACCA 1450
F C Q Q D Y N S P P T F G G G T

PCT/GB98/01627

AGCTGGAAAT CAAATAA
K L E I K .

[illegible]

Figure 3a
B7-1.5T4.1

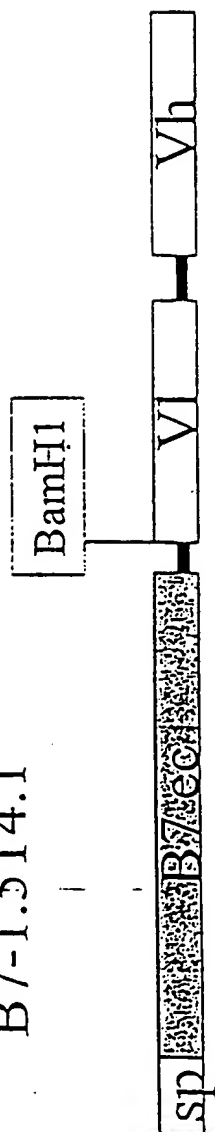
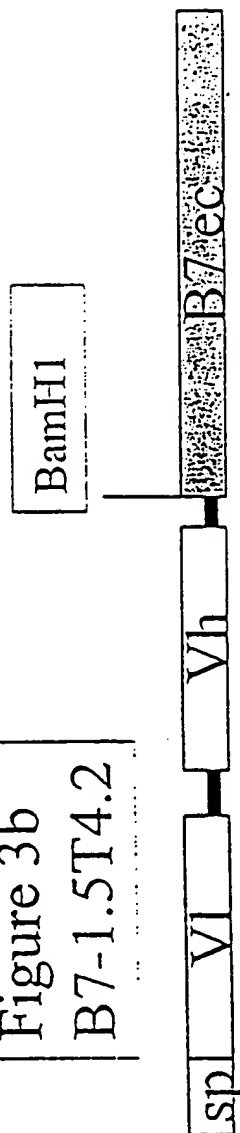


Figure 3b
B7-1.5T4.2



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Figure 4 seq id No. 4.

Molecule Name-: B7-2(1-241)
Sequence Printed: 1-738 (Full)
Description:

738 bps DNA Linear
Date Printed 02 Jun 1997

1 ATGGGACTGA GTAACATTCT CTTTGTGATG GCCTTCCTGC TCTCTGGTGC
M G L S N I L F V M A F L L S G A

51 TGCTCCTCTG AAGATTCAAG CTTATTTCAA TGAGACTGCA GACCTGCCAT
A P L K I Q A Y F N E T A D L P

101 GCCAATTTGC AAACCTCTCAA AACCAAAGCC TGAGTGAGCT AGTAGTATTT
C Q F A N S Q N Q S L S E L V V F

151 TGGCAGGACC AGGAAACTT GGTTCCTGAAT GAGGTATACT TAGGCAAAGA
W Q D Q E N L V L N E V Y L G K E

201 GAAATTTGAC AGTGTTCATT CCAAGTATAT GGGCCGCACA AGTTTTGATT
K F D S V H S K Y M G R T S F D

251 CGGACAGTTG GACCCTGAGA CTTCAACAATC TTCAGATCAA GGACAAGGGC
S D S W T L R L H N L Q I K D K G

301 TTGTATCAAT GTATCATCCA TCACAAAAG CCCACAGGAA TGATTGCGAT
L Y Q C I I H H K K P T G M I R I

351 CCACCAGATG AATTCTGAAC TGTCAGTGCT TGCTAACTTC AGTCAACCTG
H Q M N S E L S V L A N F S Q P

401 AAATAGTACC AATTTCTAAT ATAACAGAAA ATGTGTACAT AAATTTGACC
E I V P I S N I T E N V Y I N L T

451 TGCTCATCTA TACACGGTTA CCCAGAACCT AAGAAGATGA GTGTTTTGCT
C S S I H G Y P E P K K M S V L L

501 AAGAACCAAG AATTCACATA TCGAGTATGA TGGTATTATG CAGAAATCTC
R T K N S T I E Y D G I M Q K S

551 AAGATAATGT CACAGAACTG TACGACGTTT CCATCAGCTT GTCTGTTTCA
Q D N V T E L Y D V S I S L S V S

601 TTCCCTGATG TTACGAGCAA TATGACCATC TTCTGTATTC TGGAAACTGA
F P D V T S N M T I F C I L E T D

651 CAAGACGCGG CTTTATCTT CACCTTTCTC TATAGAGCTT GAGGACCCTC
K T R L L S S P F S I E L E D P

